

Genome assemblies of *Fusarium oxysporum* f. sp. *lini* strains of different virulence

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Materials

- *Fusarium oxysporum* f. sp. *lini* is one of the most dangerous pathogens causing flax wilt
- Flax is a source of high-quality fiber and an important oilseed crop
- The purpose of this study was to obtain and analyze genomes of *F. oxysporum* f. sp. *lini* strains of different degrees of pathogenicity
- The following strains of *F. oxysporum* f. sp. *lini* were used as material:
 1. low virulence (strains #456, #482)
 2. medium virulence (strains #476, #525)
 3. high virulence (strain #483, and previously sequenced isolate #39)



DNA library preparation and genome sequencing

To obtain high-quality genome assemblies, sequencing was performed on two platforms:

1. Oxford Nanopore Technologies MinION was used for obtaining long reads

- DNA extraction (modified CTAB method) and additional purification (Blood & Cell Culture DNA Mini Kit)
- Removal of DNA fragments up to 10 kb (Short Read Eliminator Kit)
- Library preparation (SQK-LSK109 and EXP-NBD103 kits)
- Sequencing with a FLO-MIN-106 (R9.4.1) flow-cell



2. Illumina MiSeq was used for obtaining high precision short reads

- For the library preparation extracted DNA was sheared and size selected, then NEBNext Ultra II DNA Library Prep Kit for Illumina was used



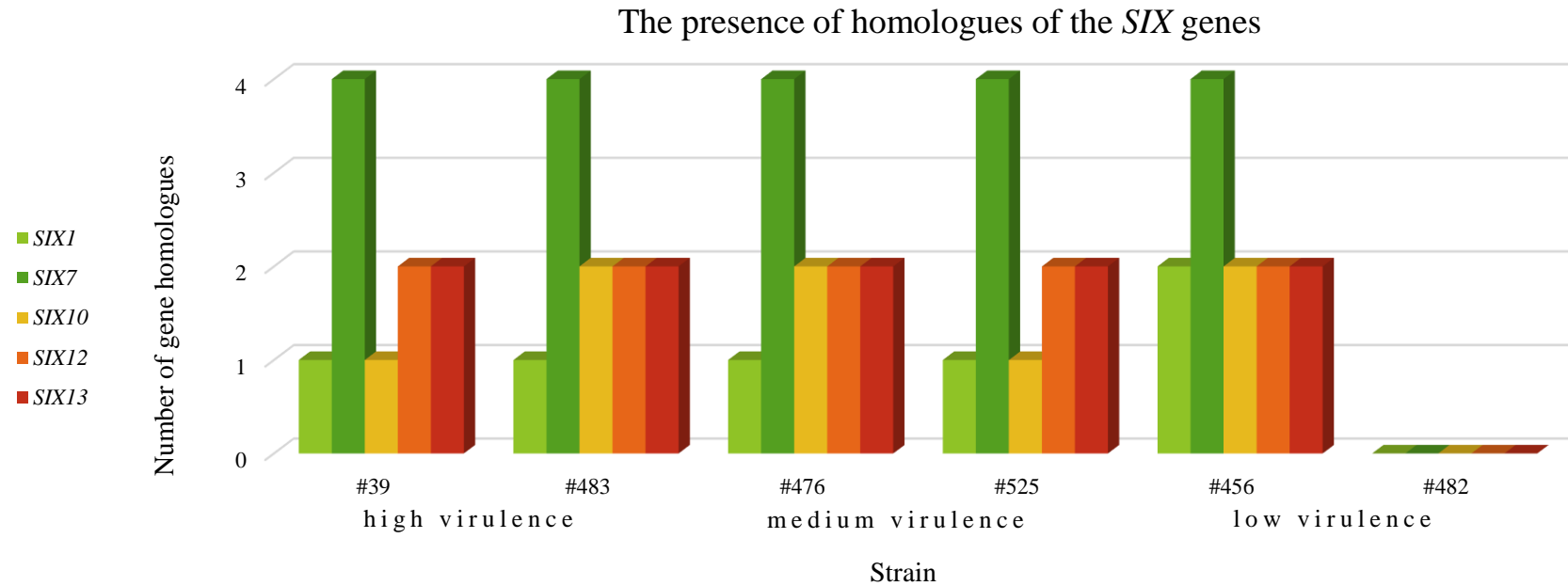
De novo genome assembly

- As a result of the sequencing on the Nanopore platform, 374-756 Mb (N50 = 32-44 kb) per strain were obtained
- As a result of the sequencing on the Illumina platform, 2.9-7.9 million 300+300 bp reads per strain were obtained
- Based on the data obtained from Nanopore and Illumina platforms, as well as reads of highly pathogenic isolate #39 obtained earlier, the genomes of 6 strains were assembled with the MaSuRCA-CA hybrid assembler
- The lengths of the assemblies were in the range of 53-69 Mb, N50 values – 1.0-2.5 Mb, and the BUSCO completeness – 96.5-99.7%

Strain	#482	#456	#525	#476	#483	#39
Virulence	low		medium		high	
Nanopore data volume, Gb	0.76	0.38	0.37	0.59	0.56	4.87
Illumina data volume, Gb	3.22	4.76	3.00	3.32	1.72	1.78
Assembly length, Mb	53.4	61.7	63.1	65.9	63.8	69.3
N50, Mb	2.4	1.1	1.0	2.5	1.6	2.3
Number of contigs	43	113	123	67	97	74
L50	7	17	21	9	11	5
GC content, %	47.30	47.86	48.11	47.87	47.98	48.07
BUSCO completeness, %	99.7	96.5	98.2	99.1	98.4	99.7

Secreted in xylem genes

SIX genes are associated with the pathogenicity of *F. oxysporum*



Gene clusters

#39, 476, 456	<i>SIX7</i>	<i>SIX1</i>		
#39, 456, 476, 483, 525	<i>SIX7</i>	<i>SIX12</i>		
#39, 456, 476, 483, 525	<i>SIX13</i>	<i>SIX7</i>	<i>SIX10</i>	
#39, 456, 476, 483, 525	<i>SIX13</i>	<i>SIX7</i>	<i>SIX12</i>	<i>SIX10</i>

The received data helps to understand the virulence mechanisms of *F. oxysporum* f. sp. *lini* and the interaction between the pathogen and flax